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Field: Title/Abstract, Limits: Publication Date to 2002

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#19	Search leuconostoc dehydrogenase Field: Title/Abstract, Limits: Publication Date to 2002	09:44:09	<u>92</u>
#16	Search leuconostoc oxidoreductase Field: Title/Abstract, Limits: Publication Date to 2002	09:38:38	<u>3</u>
#15	Search leuconostoc reductase Field: Title/Abstract, Limits: Publication Date to 2002	09:38:28	<u>2</u>
#13	Search leuconostoc mesenteroides reductase Field: Title/Abstract, Limits: Publication Date to 2002	09:34:13	<u>2</u>
#12	Search leuconostoc mesenteroides Field: Title/Abstract, Limits: Publication Date to 2002	09:34:07	<u>465</u>
#2	Search leuconostoc mesenteroides	09:33:59	<u>575</u>
#3	Search leuconostoc mesenteroides dextranicum	09:32:34	<u>21</u>
#1	Search leuconostoc	09:30:24	<u>1459</u>

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Feb 6 2006 04:30:54

DeMoss, R. Triphosphopyridine nucleotide-specific ethanol
dehydrogenase from *Leuconostoc mesenteroides*. *Bacteriol. Proc.*
(1953) 81.

3

Database : A_Geneseq_21:*
 1: geneseqp1980s:*
 2: geneseqp1990s:*
 3: geneseqp2000s:*
 4: geneseqp2001s:*
 5: geneseqp2002s:*
 6: geneseqp2003as:*
 7: geneseqp2003bs:*
 8: geneseqp2004s:*
 9: geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	% Query		Match	Length	DB	ID	Description
	Score	Match					
1	1605	100.0	317	8	ADH01242	Adh01242	Alpha-ket
2	595	37.1	319	7	ADC96588	Adc96588	E. faeciu
3	593.5	37.0	312	9	ADV16664	Adv16664	E. faeciu
4	593.5	37.0	326	7	ADC95776	Adc95776	E. faeciu
5	575.5	35.9	312	5	ABB54660	Abb54660	Lactococc
6	559	34.8	345	7	ADH86803	Adh86803	Enterococ
7	558.5	34.8	301	8	ADM93781	Adm93781	Enterococ
8	551.5	34.4	302	9	ADV16488	Adv16488	E. faecal

RESULT 1

ADH01242

ID ADH01242 standard; protein; 317 AA.

XX

AC ADH01242;

XX

DT 15-APR-2004 (first entry)

XX

DE Alpha-keto acid reductase protein, SEQ ID No 2.

XX

KW alpha-keto acid reductase; (R)-alpha-hydroxy acid;

KW beta-nicotinamide adenine dinucleotide; 2-chlorophenyl glyoxylic acid;

KW (R)-2-chloromandelic acid; alpha-hydroxy acid; mandelic acid;

KW anti-platelet agent; anti-obesity; pesticide.

XX

OS *Leuconostoc mesenteroides*.

XX

PN EP1382674-A2.

XX

PD 21-JAN-2004.

XX

PF 16-JUL-2003; 2003EP-00016163.

XX

PR 16-JUL-2002; 2002JP-00207507.

XX

PA (DAIL) DAICEL CHEM IND LTD.

XX

PI Kimoto N, Yamamoto H;

XX

DR WPI; 2004-111491/12.

DR N-PSDB; ADH01241.

XX

PT Novel alpha-keto acid reductase which reduces alpha-keto acid to produce

PT alpha-hydroxy acid using reduced beta-nicotinamide adenine dinucleotide

PT as a coenzyme, useful for producing optically active alpha-hydroxy acid.

XX

PS Claim 6; SEQ ID NO 2; 48pp; English.

XX

CC The invention relates to a novel alpha-keto acid reductase. The novel
 CC alpha-keto acid reductase reduces alpha-keto acid to produce (R)-alpha-
 CC hydroxy acid using reduced beta-nicotinamide adenine dinucleotide as the
 CC coenzyme; and is able to utilise reduced beta-nicotinamide adenine
 CC dinucleotide as a coenzyme in a reduction reaction, reducing 2-
 CC chlorophenyl glyoxylic acid to produce (R) 2-chloromandelic acid. The
 CC alpha-keto acid reductase is useful for producing optically active alpha-
 CC hydroxy acid and mandelic acid. The optically active mandelic acid
 CC derivatives obtained by a method of the invention are useful as
 CC intermediates in synthesizing pharmaceutical, preferably anti-platelet
 CC agents or anti-obesity drugs, and pesticides. This sequence represents
 CC the alpha-keto acid reductase protein of the invention.

XX

SQ Sequence 317 AA;

Query Match 100.0%; Score 1605; DB 8; Length 317;

Best Local Similarity 100.0%; Pred. No. 2.6e-137;

Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MKIAIAGFGALGARLGVMLQAGGHEVTGIDGWPAHIAAINTKGLTVVKDNDAPQKYFVPV	60
Db	1	MKIAIAGFGALGARLGVMLQAGGHEVTGIDGWPAHIAAINTKGLTVVKDNDAPQKYFVPV	60
Qy	61	MPASEVTGTFDLIILLTKTPQLDRMLTDIQPIITDTTKLLVLSNGLGNIEVMAKHVSRHQ	120
Db	61	MPASEVTGTFDLIILLTKTPQLDRMLTDIQPIITDTTKLLVLSNGLGNIEVMAKHVSRHQ	120
Qy	121	ILAGVTLWTSSLIKPGEIHVTGSGSIKLQAIGDADVQSIADALNQAGLNAEITPDVMTAI	180
Db	121	ILAGVTLWTSSLIKPGEIHVTGSGSIKLQAIGDADVQSIADALNQAGLNAEITPDVMTAI	180
Qy	181	WHKAGINAVLNPLSVLLNANIAEFGTAGNAMDLALNILDEMKQVGASQGIKVDVSGIMTD	240
Db	181	WHKAGINAVLNPLSVLLNANIAEFGTAGNAMDLALNILDEMKQVGASQGIKVDVSGIMTD	240
Qy	241	LSQLLKPENAGNHFFPSMYQDIQNGKRTEIDFLNGYFAKIGHESGIPTPFNALVTRLIHAK	300
Db	241	LSQLLKPENAGNHFFPSMYQDIQNGKRTEIDFLNGYFAKIGHESGIPTPFNALVTRLIHAK	300
Qy	301	EDIERVKLAKQQENFEI	317
Db	301	EDIERVKLAKQQENFEI	317

RESULT 2

ADC96588

ID ADC96588 standard; protein; 319 AA.

XX

AC ADC96588;

XX

DT 01-JAN-2004 (first entry)

XX

DE E. faecium protein sequence SEQ ID 6215.

XX

KW Vaccine; urinary tract infection; bacteraemia; endocarditis; wound;
KW abdominal-pelvic infection.

XX

OS Enterococcus faecium.

XX

PN US6583275-B1.

XX

PD 24-JUN-2003.

XX

PF 30-JUN-1998; 98US-00107532.

XX

PR 02-JUL-1997; 97US-0051571P.

PR 14-MAY-1998; 98US-0085598P.

XX

PA (GENO-) GENOME THERAPEUTICS CORP.

XX

PI Doucette-Stamm LA, Bush D;

XX

DR WPI; 2003-799836/75.

DR N-PSDB; ADC92934.

XX

PT New isolated nucleic acid derived from Enterococcus faecium encoding an

Database : Issued_Patents_AA:*
 1: /cgn2_6/ptodata/1/iaa/5_COMB.pep:*
 2: /cgn2_6/ptodata/1/iaa/6_COMB.pep:*
 3: /cgn2_6/ptodata/1/iaa/H_COMB.pep:*
 4: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
 5: /cgn2_6/ptodata/1/iaa/RE_COMB.pep:*
 6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	%		Query			Description
	Score	Match	Length	DB	ID	
1	595	37.1	319	2	US-09-107-532A-6215	Sequence 6215, Ap
2	593.5	37.0	326	2	US-09-107-532A-5403	Sequence 5403, Ap
3	559	34.8	345	2	US-09-134-000C-4688	Sequence 4688, Ap
4	474	29.5	279	2	US-09-134-000C-5430	Sequence 5430, Ap
5	461.5	28.8	313	2	US-09-710-279-2568	Sequence 2568, Ap
6	461.5	28.8	317	2	US-09-134-001C-3366	Sequence 3366, Ap
7	460	28.7	243	2	US-09-134-000C-3753	Sequence 3753, Ap
8	254.5	15.9	306	2	US-09-489-039A-13474	Sequence 13474, A
9	219.5	13.7	315	2	US-09-252-991A-24352	Sequence 24352, A
10	211.5	13.2	320	2	US-09-543-681A-6146	Sequence 6146, Ap
11	198	12.3	281	2	US-09-902-540-11701	Sequence 11701, A
12	174.5	10.9	358	2	US-09-248-796A-15976	Sequence 15976, A
13	173.5	10.8	319	2	US-09-252-991A-30187	Sequence 30187, A
14	170	10.6	359	2	US-09-538-092-111	Sequence 111, App
15	158.5	9.9	300	2	US-09-710-279-1420	Sequence 1420, Ap

Database : Published_Applications_AA_Main:*

- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
- 2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
- 3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
- 4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
- 5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
- 6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	8 Query		Length	DB	ID	Description
	Score	Match				
1	1605	100.0	317	4	US-10-619-779-2	Sequence 2, Appli
2	461.5	28.8	317	4	US-10-724-972A-4872	Sequence 4872, Ap
3	248	15.5	300	3	US-09-738-626-4711	Sequence 4711, Ap
4	243.5	15.2	323	4	US-10-156-761-9372	Sequence 9372, Ap
5	183	11.4	298	5	US-10-984-449-30	Sequence 30, Appl
6	158.5	9.9	317	4	US-10-724-972A-5107	Sequence 5107, Ap
7	155.5	9.7	72	4	US-10-424-599-249547	Sequence 249547,
8	127.5	7.9	514	4	US-10-282-122A-45523	Sequence 45523, A
9	123	7.7	318	4	US-10-156-761-13346	Sequence 13346, A
10	121.5	7.6	429	4	US-10-369-493-14884	Sequence 14884, A
11	121.5	7.6	430	4	US-10-369-493-11682	Sequence 11682, A
12	121.5	7.6	430	4	US-10-369-493-14339	Sequence 14339,

Database : PIR_80:*
 1: pir1:*
 2: pir2:*
 3: pir3:*
 4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query		DB	ID	Description
		Match	Length			
1	724	45.1	305	2	AC0828	probable oxidoredu
2	575.5	35.9	312	2	C86790	2-dehydropantoate
3	497.5	31.0	311	2	D90046	hypothetical prote
4	349.5	21.8	307	2	D97261	ketopantoate reduc
5	340.5	21.2	301	2	H71011	probable thiamin b
6	317.5	19.8	300	2	H75119	probable 2-dehydro
7	314	19.6	310	2	A70449	hypothetical prote
8	311.5	19.4	294	2	F69461	thiamin biosynthes
9	268.5	16.7	296	2	D82092	2-dehydropantoate
10	263	16.4	303	2	D84230	hypothetical prote
11	255.5	15.9	303	2	AC0385	2-dehydropantoate
12	248.5	15.5	337	2	T31129	hypothetical prote
13	242.5	15.1	323	2	T35004	probable oxidoredu
14	239.5	14.9	303	2	G90688	hypothetical prote
15	239.5	14.9	303	2	C85539	hypothetical prote
16	235.5	14.7	303	2	A64772	ketopantoate reduc
17	233	14.5	301	2	A97098	ketopantoate reduc
18	226.5	14.1	303	2	E83096	ketopantoate reduc

Database : UniProt_05.80:*
 1: uniprot_sprot:*
 2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	726	45.2	305	2	Q5PIJ0_SALPA	Q5pij0 salmonella
2	724	45.1	305	2	Q8Z4L0_SALTI	Q8z4l0 salmonella
3	723	45.0	305	2	Q8ZN23_SALTY	Q8zn23 salmonella
4	714	44.5	305	2	Q57LD8_SALCH	Q57ld8 salmonella
5	613.5	38.2	308	2	Q8XMA4_CLOPE	Q8xma4 clostridium
6	603	37.6	313	2	Q831Q5_ENTFA	Q831q5 enterococcu
7	591.5	36.9	312	2	Q8KUB0_ENTFA	Q8kub0 enterococcu
8	575.5	35.9	312	1	PANE_LACLA	Q9cfy8 lactococcus
9	559	34.8	313	2	Q834J5_ENTFA	Q834j5 enterococcu
10	551	34.3	307	2	Q8DYX1_STRA5	Q8dyx1 streptococc
11	551	34.3	307	2	Q8E4I0_STRA3	Q8e4i0 streptococc
12	541	33.7	307	1	PANE_STRP3	P65667 streptococc
13	541	33.7	307	1	PANE_STRPY	P65666 streptococc
14	538	33.5	307	1	PANE_STRP6	Q5xcq0 streptococc
15	538	33.5	307	1	PANE_STRP8	Q8p1f1 streptococc
16	501.5	31.2	311	2	Q8NUZ2_STAAB	Q8nuz2 staphylococ
17	501.5	31.2	311	2	Q5HDB0_STAAC	Q5hdb0 staphylococ
18	497.5	31.0	311	2	Q7A3Q3_STAAN	Q7a3q3 staphylococ
19	497.5	31.0	311	2	Q99RI8_STAAM	Q99ri8 staphylococ
20	494.5	30.8	311	2	Q6G6M7_STAAS	Q6g6m7 staphylococ
21	492.5	30.7	311	2	Q6GDY9_STAAR	Q6gdy9 staphylococ
22	487.5	30.4	310	2	Q4L8V1_STAHJ	Q4l8v1 staphylococ
23	461.5	28.8	310	2	Q5HLG5_STAEQ	Q5hlg5 staphylococ
24	461.5	28.8	310	2	Q8CN57_STAEP	Q8cn57 staphylococ
25	448.5	27.9	307	2	Q4KB04_PSEF5	Q4kb04 pseudomonas
26	422	26.3	309	2	Q4PJB5_9BACT	Q4pjb5 uncultured
27	420	26.2	222	2	Q83Z94_ENTFA	Q83z94 enterococcu
28	411	25.6	310	2	Q63WP8_BURPS	Q63wp8 burkholderi
29	405	25.2	313	2	Q62MA2_BURMA	Q62ma2 burkholderi
30	400	24.9	314	2	Q4LLS8_9BURK	Q4lls8 burkholderi
31	382	23.8	308	2	Q4JML1_9BACT	Q4jml1 uncultured
32	369	23.0	332	2	Q64D62_9ARCH	Q64d62 uncultured

RESULT 2

Q8Z4L0_SALTI

ID Q8Z4L0_SALTI PRELIMINARY; PRT; 305 AA.
AC Q8Z4L0; Q7CBM3;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE Putative oxidoreductase.
GN OrderedLocusNames=STY2819, t0284;
OS Salmonella typhi.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Salmonella.
OX NCBI_TaxID=601;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=CT18;
RX MEDLINE=21534947; PubMed=11677608; DOI=10.1038/35101607;
RA Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J.,
RA Churcher C.M., Mungall K.L., Bentley S.D., Holden M.T.G., Sebaihia M.,
RA Baker S., Basham D., Brooks K., Chillingworth T., Connerton P.,
RA Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J.,
RA Feltwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagels K.,
RA Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C.,
RA Quail M.A., Rutherford K.M., Simmonds M., Skelton J., Stevens K.,
RA Whitehead S., Barrell B.G.;
RT "Complete genome sequence of a multiple drug resistant Salmonella
RT enterica serovar Typhi CT18.";
RL Nature 413:848-852(2001).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Ty2 / ATCC 700931;
RX MEDLINE=22531367; PubMed=12644504;
RX DOI=10.1128/JB.185.7.2330-2337.2003;
RA Deng W., Liou S.-R., Plunkett G. III, Mayhew G.F., Rose D.J.,
RA Burland V., Kodoyianni V., Schwartz D.C., Blattner F.R.;
RT "Comparative genomics of Salmonella enterica serovar Typhi strains Ty2
RT and CT18.";
RL J. Bacteriol. 185:2330-2337(2003).
DR EMBL; AL627275; CAD02775.1; -; Genomic_DNA.
DR EMBL; AE016835; AAO68009.1; -; Genomic_DNA.
DR GO; GO:0008677; F:2-dehydropantoate 2-reductase activity; IEA.
DR GO; GO:0016491; F:oxidoreductase activity; IEA.
DR GO; GO:0015940; P:pantothenate biosynthesis; IEA.
DR GO; GO:0006206; P:pyrimidine base metabolism; IEA.
DR InterPro; IPR003710; ApbA.
DR InterPro; IPR000205; NAD_BS.
DR Pfam; PF02558; ApbA; 1.
DR TIGRFAMS; TIGR00745; apbA_panE; 1.
KW Complete proteome.
SQ SEQUENCE 305 AA; 33123 MW; 67FD347DB3D1E58F CRC64;

Query Match 45.1%; Score 724; DB 2; Length 305;
Best Local Similarity 48.2%; Pred. No. 8.7e-45;
Matches 147; Conservative 51; Mismatches 101; Indels 6; Gaps 3;

Qy 1 MKIAIAGFGALGARLGVMQAGGHEVTGIDGWPAHIAAINTKGLTVVKDNDAPQKYF-VP 59
||||| ||:| | | || ||:|| |||| |: || :|| | : : |||: :|

RESULT 3

Q8ZN23_SALTY

ID Q8ZN23_SALTY PRELIMINARY; PRT; 305 AA.
 AC Q8ZN23;
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Putative ketopantoate reductase (EC 1.1.1.169).
 GN OrderedLocusNames=STM2573;
 OS Salmonella typhimurium.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Salmonella.
 OX NCBI_TaxID=602;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=LT2 / SGSC1412 / ATCC 700720;
 RX MEDLINE=21534948; PubMed=11677609; DOI=10.1038/35101614;
 RA McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P.,
 RA Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D.,
 RA Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E.,
 RA Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M.,
 RA Waterston R., Wilson R.K.;
 RT "Complete genome sequence of Salmonella enterica serovar Typhimurium
 RT LT2.";
 RL Nature 413:852-856(2001).
 DR EMBL; AE008817; AAL21467.1; -; Genomic_DNA.
 DR GO; GO:0008677; F:2-dehydropanoate 2-reductase activity; IEA.
 DR GO; GO:0016491; F:oxidoreductase activity; IEA.
 DR GO; GO:0015940; P:pantothenate biosynthesis; IEA.
 DR GO; GO:0006206; P:pyrimidine base metabolism; IEA.
 DR InterPro; IPR003710; ApbA.
 DR InterPro; IPR000205; NAD_BS.
 DR Pfam; PF02558; ApbA; 1.
 DR TIGRFAMs; TIGR00745; apbA_panE; 1.
 KW Complete proteome; Oxidoreductase.
 SQ SEQUENCE 305 AA; 33150 MW; 67FD347DAB72E58F CRC64;

Query Match 45.0%; Score 723; DB 2; Length 305;
 Best Local Similarity 48.2%; Pred. No. 1e-44;
 Matches 147; Conservative 51; Mismatches 101; Indels 6; Gaps 3;

Qy 1 MKIAIAGFGALGARLGVMQLQAGGHEVTGIDGWPAHIAAINTKGLTVVKDNDAPQKYF-VP 59
 ||||| ||:| | | || ||:| | || | : || :|| | : : ||| : |
 Db 1 MKIAIAGAGAMGCRFGYMLLEAGHDVTLIDGWQEHVDAIRSKGLFV--ETETTKQKYPIPI 58
 Qy 60 VMPASEVTGTFDLIILLTKTPQLDRMLTDIQPIITDTTKLLVLSNGLGNIEVMAKHVSRH 119
 | | | | :|:| | | || | | | :|:| :|:| | | : | : | |
 Db 59 AMLADESQGEFELVILFTKAMQLDSMLQRIKPLLPAKVVMILSNGLGNIEVMAKHVSRH 118
 Qy 120 QILAGVTLWTSSLIKPGIEHVTGSGSIKLQAIQDAD---VQSIADALNQAGLNAEITPDV 176
 : | ||||| : | | | | :|:|:| | | | : | | ||||| : |||
 Db 119 KIYAGVTLWSSELEGAGHIMATGTGTIELQPIASQDSAEAKVIATLNSAGLNAEISPDV 178
 Qy 177 MTAIWHKAGINAVLNPLSVLLNANIAEFGTAGNAMDALNILDENKQVGASQGIKVDVSG 236
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 Db 179 LLSIWKKAAFNSVMNTYCALLDCNVGGFGQRPGLDLAQAVVDEFVLVAASQNIPLTEQM 238

Qy 237 IMTDLSQLLKPENAGNHFPSMYQDIQNGKRTEIDFLNGYFAKIGHESGIPTPFNALVTRL 296
:| : :: | :|:|:|:|:|: |: | |:|:|:| |:| : : | | | |:|:|
Db 239 VMNTVKKVFDPRESGHHYPSMHQDLHKGRLTEIDYLNCAIARIGAQNNIAPVNVKLLTQL 298
Qy 297 IHAKE 301
| | | | |
Db 299 IHAKE 303

RESULT 1

US-09-107-532A-6215

; Sequence 6215, Application US/09107532A

; Patent No. 6583275

; GENERAL INFORMATION:

; APPLICANT: Lynn A Doucette-Stamm and David Bush

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND

THERAPEUTICS

; NUMBER OF SEQUENCES: 7310

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: GENOME THERAPEUTICS CORPORATION

; STREET: 100 Beaver Street

; CITY: Waltham

; STATE: Massachusetts

; COUNTRY: USA

; ZIP: 02354

; COMPUTER READABLE FORM:

; MEDIUM TYPE: CD-ROM ISO9660

; COMPUTER: PC

; OPERATING SYSTEM: <Unknown>

; SOFTWARE: ASCII

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/107,532A

; FILING DATE: 30-Jun-1998

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 60/085,598

; FILING DATE: 14 May 1998

; APPLICATION NUMBER: 60/051571

; FILING DATE: July 2, 1997

; ATTORNEY/AGENT INFORMATION:

; NAME: Ariniello, Pamela Deneke

; REGISTRATION NUMBER: 40,489

; REFERENCE/DOCKET NUMBER: GTC-012

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (781)893-5007

; TELEFAX: (781)893-8277

; INFORMATION FOR SEQ ID NO: 6215:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 319 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; HYPOTHETICAL: YES

; ORIGINAL SOURCE:

; ORGANISM: Enterococcus faecium

; FEATURE:

; NAME/KEY: misc_feature

; LOCATION: (B) LOCATION 1...319

; SEQUENCE DESCRIPTION: SEQ ID NO: 6215:

US-09-107-532A-6215

Query Match 37.1%; Score 595; DB 2; Length 319;

Best Local Similarity 41.3%; Pred. No. 7.5e-51;

Matches 128; Conservative 57; Mismatches 117; Indels 8; Gaps 4;

Qy 1 MKIAIAGFGALGARLGVMLQAGGHEVTGIDGWPAAHIAAINTKGLTVVKDNDAPQKYFVPV 60

Db	7	: : : : : : : :	
		MKIAIAGAGAMGSRIGMLHQSGNEVLLIDRWPAHIEAIRTNGL-IADFNQKEVVAKLPI	65
Qy	61	MPASEVTGT---FDLIILLTKTPQLDRMLTDIQPIITDTTKLLVLSNGLGNIEVMAKHVS	117
		: : : : : : :	
Db	66	YSPEEIIIESNEHVDLIVALTKANQLDDMFCSIQSIITDNTYVLCLLNGLGHEDVLEKYVP	125
Qy	118	RHQILAGVTLWTSSSLIKPGEIHVTGSGSIKLQAI---GDADVQSIADALNQAGLNAEITP	174
		: : : : :: : : : : : : : : : :	
Db	126	KKNILFGITMWTAGLAGPGKVTL LGDGEIELENLEPEGEAFTKKVVEVFQEANLNPIYSH	185
Qy	175	DVMTAIWHKAGINAVLNPLSVLLNANIAEFGTAGNAMDLALNILDENKQVGASQGIKVDV	234
		: : : : : : : : : :	
Db	186	NVRYSIWRKACVNGTLNGLCTILDCNIAELGAQKAAESMVRTIVSEFASIAAKEGIILDQ	245
Qy	235	SGIMTDLSQLLKPENAGNHFPSPYQD-IQNGKRTEIDFLNGYFAKIGHESGIPTPFNALV	293
		: : : : : : : : : : : :	
Db	246	EEVYQHIASTYDPDNIGLHYPSMYQDLIKNHLRLTEIDYINGAIWRKGQKYDIATPYCAFL	305
Qy	294	TRLIHAKEDI	303
		: :	
Db	306	TQLVHAKEGI	315